

Notch (C)	IDE \bar{C} -SNP	\bar{C} QNGGTC---D-V \bar{G} SY- \bar{C} -CP \bar{P} GFT	GK--- \bar{C} E-N
<u>10244 (C)</u>	-NE \bar{C} TM---	\bar{C} QH--- \bar{C} VNT- \bar{G} SY- \bar{C} K \bar{C} -S \bar{G} --	\bar{G} --L- \bar{C} D
80		\bar{C} R \bar{C} FP \bar{G} YT	\bar{G} KT \bar{C} SQ D
95	VNE \bar{C} GKMPRP	\bar{C} QHR \bar{C} VNT \bar{H} \bar{G} SYK \bar{C} F \bar{C} LS	\bar{G} HMLMP D
133	VNSRTCAMIN	\bar{C} QYS \bar{C} EDT \bar{E} GPQ \bar{C} L \bar{C} PSS	\bar{G} LRLAPN
175	IDE \bar{C} ASGKVI	\bar{C} PYNRR \bar{C} VNT \bar{F} \bar{G} SY \bar{C} K \bar{C} HIGFE	LQYISGR
220	INE \bar{C} TMDSHT	\bar{C} SHHAN \bar{C} FNTQGSF \bar{C} K \bar{C} KQ \bar{G} YK	\bar{G} NGRL \bar{C} S
<u>CD97 (C)</u>	V-E \bar{C} -SG-Q-- \bar{C} -SS-- \bar{C}	-NTV \bar{G} SY- \bar{C} R \bar{C} RP \bar{G} W-P-P \bar{G} -PN---	D
<u>EGF (C)</u>	NSDSE \bar{C} PLSHDGY \bar{C} LHDGV \bar{C} MYIEALDKYA \bar{C} NCV \bar{G} YI---	\bar{G} ER-- \bar{C} QYRDLLKWWELR	

Figure 1

09981649.022802

GGCTGGAGAA GAAACAGCAA GGGAGTCTGT GAAGCTACAT GCGAACCTGG
 ATGTAAGTTT GGTGAGTGCG TGGGACCAAA CAAATGCAGA TGCTTTCCAG
 GATACACCGG GAAAACCTGC AGTCAAGATG TGAATGAGTG TGGAATGAAA
 CCCC GGCCAT GCCAACACAG ATGTGTGAAT ACACACGGAA GCTACAAGTG
 CTTTTGCCTC AGTGGCCACA TGCTCATGCC AGATGCTACG TGTGTGAACT
 CNAGGACATG TGCCATGATA AACTGTCAGT ATAGCTGTGA AGACACAGAA
 SEQ ID NO: 1

GGCTGGAGAA GAAACAGCAA GGGAGTCTGT GAAGCTACAT GCGAACCTGG
 ATGTAAGTTT GGTGAGTGCG TGGGACCAAA CAAATGCAGA TGCTTTCCAG
 GATACACCGG GAAAACCTGC AGTCAAGATG TGAATGAGTG TGGAATGAAA
 CCCC GGCCAT GCCAACACAG ATGTGTGAAT ACACACGGAA GCTACAAGTG
 CTTTTGCCTC AGTGGCCACA TGCTCATGCC AGATGCTACG TGTGTGAACT
 CNAGGACATG TGCCATGATA AACTGTCAGT ATAGCTGTGA AGACACAGAA
 GAAGGGCCAC AGTGCCTGTG TCCATCCTCA GGACTCCGCC TGGCCCCAAA
 TGGAAGAGAC TGTCTAGATA TTGATGAATG TGCCTCTGGT AAAGTCATCT
 GTCCCTACAA TCGAAGATGT GTGAACACAT TTGGAAGCTA CTA CTGCAAAA
 TGTCACATTG GTTTCGAACT GCAATATATC AGTGGACGAT ATGACTGTAT
 AGATATAAAT GAATGTACTA TGGATAGCCA TACGTGCAGC CACCATGCCA
 ATTGCTTCAA TACCCAAGGG TCCTTCAAGT GTAAATGCAA GCAGGGATAT
 AAAGGCAATG GACTTCGGTG TTCTGCTATC CCTGAAAATT CTGTGAAGGA
 AGTCCTCAGA GCACCTGGTA CCATCAAAGA CAGAATCAAG AAGTTGCTTG
 CTCACAAAAA CAGCATGAAA AAGAAGGCAA AAATTAAAAA TGT TACCCCA
 GAACCCACCA GGACTCCTAC CCCTAAGGTG AACTTGCAGC CTTCAACTA
 TGAAGAGATA GTTTCAGAG GCGGGAACCTC TCATGGAGGT AAAAAAGGGA
 ATGAAGAGAA AATGAAAGAG GGGCTTGAGG ATGAGAAAAG AGAAGAGAAA
 GCCCTGAAGA ATGACATAGA GGAGCGAAGC CTGCGAGGAG ATGTGTTTTT
 CCCTAAGGTG AATGAAGCAG GTGAATTCGG CCTGATTCTG GTCCAAAGGA
 AAGCGCTAAC TTCCAAACTG GAACATAAAG ATTTAAATAT CTCGGTTGAC
 TGCAGCTTCA ATCATGGGAT CTGTGACTGG AAACAGGATA GAGAAGATGA
 TTTTGACTGG AATCCTGCTG ATCGAGATAA TGCTATTGGC TTCTATATGG
 CAGTTCCGGC CTTGGCAGGT CACATGAAAG ACATTGGCCG ATTGAAACTT
 CTCCTACCTG ACCTGCAACC CCAAAGCAAC TTCTGTTTGC TCTTTGATTA
 CCGGCTGGCC GGAGACAAAG TCGGGAAACT TCGAGTGTTT GTGAAAAACA
 GTAACAATGC CCTGGCATGG GAGAAGACCA CGAGTGAGGA TGAAAAGTGG
 AAGACAGGGA AAATTCAGTT GTATCAAGGA ACTGATGCTA CCAAAGCAT
 CATTTTTGAA GCAGAACGTG GCAAGGGCAA AACC GGCGAA ATCGCAGTGG
 ATGGCGTCTT GCTTGTTTCA GGCTTATGTC CAGATAGCCT TTTATCTGTG
 GANNNCTGAA TGGTACTATC TTTATATTTG ACTTTGTATG TCAGTTCCTT
 GGTTTTTTTTG ATATTGCATC ATAGGACCTC TGGCATTTTA AAATTACTAG
 CTGAAAAATT G
 SEQ ID NO: 2

FIGURE 2

GWRRNSKGVCEATCEPGCKFGECVGPNNKCRCFPGYTGKTCSQDVNECGMKPRPCQHR
CVNTHGSYKCFCLSGHMLMPDATCVNSRTCAMINCQYSCEDTE
SEQ ID NO:3

GWRRNSKGVCEATCEPGCKFGECVGPNNKCRCFPGYTGKTCSQDVNECGMKPRPCQHR
CVNTHGSYKCFCLSGHMLMPDATCVNSRTCAMINCQYSCEDTEEGPQCLCPSSGLRLAP
NGRDCLDIDECASGKVICPYNRRVCNTFGSYCKCHIGFELQYISGRYDCIDINECTMDS
HTCSHHANCFNTQGSFKCKCKQGYKGNGLRCSAIPENSVKEVLRAPGTIKDRIKKLLAH
KNSMKKKAKIKNVTPEPTRTPTPKVNLQPFNYEEIVSRGGNSHGGKKGNEEKMKEGLE
DEKREEKALKNDIEERSLRGDVFFPKVNEAGEFGLILVQRKALTSLKLEHKDLNISVDCSF
NHGICDWKQDREDDFDWNPADRDNAIGFYMAVPALAGHMKDIGRLKLLLPDLQPQSN
FCLLFDYRLAGDKVGKLRVFKNSNNALAWKTTSEDEKWKTGKIQLYQGTDATKSIIF
EAERGKGTGEIAVDGVLLVSGLCPSLLSVDDXMVLSLYLTLYVSSLVFLILHRTSGI
LKLLAEKL
SEQ ID NO:4

FIGURE 3

09981649.022802

20220" 54513650

ACTAGTGATTCCATCTAATACGACTCACTATAGGGCTCGAGCGGCCGCCCGGCAGGTCTGCAGGGACAGCACCCCGGTA
ACTGCGAGTGGAGCGGAGGACCCGAGCGGCTGAGGAGAGAGAGAGCGCGGCTTAGCTGCTACGGGGTCCGGCCCGCGCC
CTCCGAGGGGGCTCAGGAGGAGGAAGAGGACCCGCTGCGAGAAATGCTCTGCCCTGGAGCCTTCCGCTCCCGCTGCTG
CTCCCTGGGTGGCAGGTGGTTTCGGGAACCGGCCAGTGCAGGCATCACGGGTTGTTAGCATCGGCACGTCAGCCTGG
GGTCTGTCACTATGGAACATAAATGGCTGCTGCTACGGGTGGAGAAACAGCAAGGAGTCTGTGAAGCTACATGCGG
AACTTGGATGTAAGTTGGTGAGTGGTGGGACCAAAACAATGCAGATGCTTTCAGGATACACCGGGAAAAACCTGCAGT
CAAGATGTGAATGAGTGTGGAATGAACCCCGGCCATGCCAACACAGATGTGTGAATACACACGGAAGCTACAAGTCTT
TTGCCCTCAGTGGCCACATGCTCATGCCAGATGCTACGTGTGTGAATCTCAGGATCCGCCCTGGCCCCAAATGGAAGACTGT
GCTGTGAAGACACAGAAGAAGGCCACAGTGCCTGTGTCACTCAATCGAAGATGTGTGAACACATTTGGAAGCTACTA
CTAGATAATTGATGAATGTGCCCTCTGTAAAGTCACTGTGCCCTACAATCGAAGATGTGTGAACACATTTGGAAGCTACTA
CTGCAATGTCAATGGTTTCGAACCTGCAATATATCAGTGGACGATATGACTGTATAGATATAAATGAATGTACTATGG
ATAGCCATACGTGCAGCCACCATGCCAATTGCTTCAATACCCAGGTCTTCAAGTGAATGCAAGCAGGGATATAAA
GGCAATGGACTTCCGTGTTCTGCTATCCCTGAAATTTCTGTGAAGGAATCTCAGAGCACCTGGTACCATCAAGACAG
AATCAAGAAGTTGCTGTCTCAAAAACAGCATGAAAAGAGGCAAAATTAATAATGTTACCCAGAACCCACCCAGGA
CTCTACCCCTAAGTGAACTTGCAGCCCTTCAACTATGAAGAGATAGTTTCCAGAGGGGAACTCTCATGGAGGTAAA
AAAGGGAATGAAGAGAAAATGAAGAGGGGCTTGAGGATGAGAAAAGAGAGAGAAAAGCCCTGAAGAAATGACWTAGAGGA
GCGAAGCCTCGGAGGAGATGTGTTTTTCCCTAAGTGAATGAAGCAGGTGAATTCGGCCTGATTTCTGGTCCAAAGGAAAG
CGCTAACTTCCAACTGGAAACATAAAGATTTAAATATCTCGGTGACTGCGAGTTCAATCATGGGATCTGTGACTGGA
CAGGATAGAGAAGATGTTTGACTGGAATCTGCTGATCGAGATAATGCTATTGGCTTCTATATGGCAGTTCGGGCTT
GGCAGGTCACAAGAAAGACATTTGGCCGATTGAAACTTCTCTACCTGACCTGCAACCCCAAGCAACTTCTGTTGCTCT
TTGATTACCGGCTGGCCGAGACAAAGTCGGGAAAATTCAGTGTGTTGTGAAAAACAGTAACAATGCCCTGGCATGGGAG
AAGACACGAGTGAGGATGAAAAGTGGAAAGACAGGAAAAATTCAGTTGTATCAAGGAACTGATGCTACCAAAAGCATCAT
TTTTGAAGCAGAACCTGGCAAGGGGCAAAACCGCGGAAATCGCAGTGGATGGCTCTTGTGTTTCAGGCTTATGTCAG
ATAGCCTTTTATCTGTGGATGACTGAATGTTACTATCTTTATATTTGACTTTGTATGTACGTTCCCTGGTGTGTTTGTGATA
TTGSATCATAGGACCTCTGGCATTTTAAATTAATAAGCTGAAAAATTTGTAATGTACCAACAGAAATTTATTTGTAAGA
TGCCCTTMTTGTATAAGATATGCCAATAATTTGCTTTAAATATCATATCACTGTATCTTCTCAGTCATTTCTGAATCTTTC
CACATTATATTAATAATATGGAATGTGAGTTTATCTCCCTCCTCAGTATATCTGATTTGTATAAGTAAGTTGATGA
GCTTCTCTCTGCAACATTTCTAGAAAAATAGAAAAAAGCACAGAGAAATGTTTAACTGTTTGTACTCTTATGATAGTTT
TGGAAAACTATGACATCAAGATAGACTTTTGGCCTAAGTGGCTTTCATAGCCAAACTTGTATATTTTAAAT
TCTTTGTATAATAATATCCAAATCATCAAAAAAATAAAAAA
SEQ ID NO: 5

MPLPWSLALPLLLPWAGFGNAASARHHGLLASARQPGVCHYGTKLACCYGWRRNSKGVCEATCEPGCKFGEVGNKC
RCFPYGTGKTCSDQDNECGMKPRPCQHRQVNTGHSYKFCISGHLMPDATCVNSRTCAMINQYSCEDTEEGPQCLCPS
SGLRLAPNGRDCLDIDECASGKVICPNRRRCVNTFGSYCKCHIGFELQYISRYDCIDINECTWDSHTCSHANCENTQ
GSFKCKQGYKGNLRCSAIPENSVKEVLRAPGTIKDRIKLLAHKNSMKKAKIKNVTPEPTPTPKVNLQPFNYEE
IVSRGNSHGGKKGNEKMEGLEDEKREEKALKNDXEERSLRGDVFFPKVNEAGEFGLILVQRKALTSKLEHKDLNISV
DCSFNHGICDWKQDREDDFDWNPADRDNAIGFYMAVPALAGHKDIGRLKLLLPDLQPOSFCLLPDYRLAGDKVGLRV
FVKNSNALAWKTTTSEDEKWKTKIQLYQGTDAKSIIFEAERGKGTGEIATVDGVLLVSLGLCPDLSLLSVDD

SEQ ID NO: 6

FIGURE 4

**EGFL6 (221-260 aa)
3D Model**

**EGF
NMR Structure**

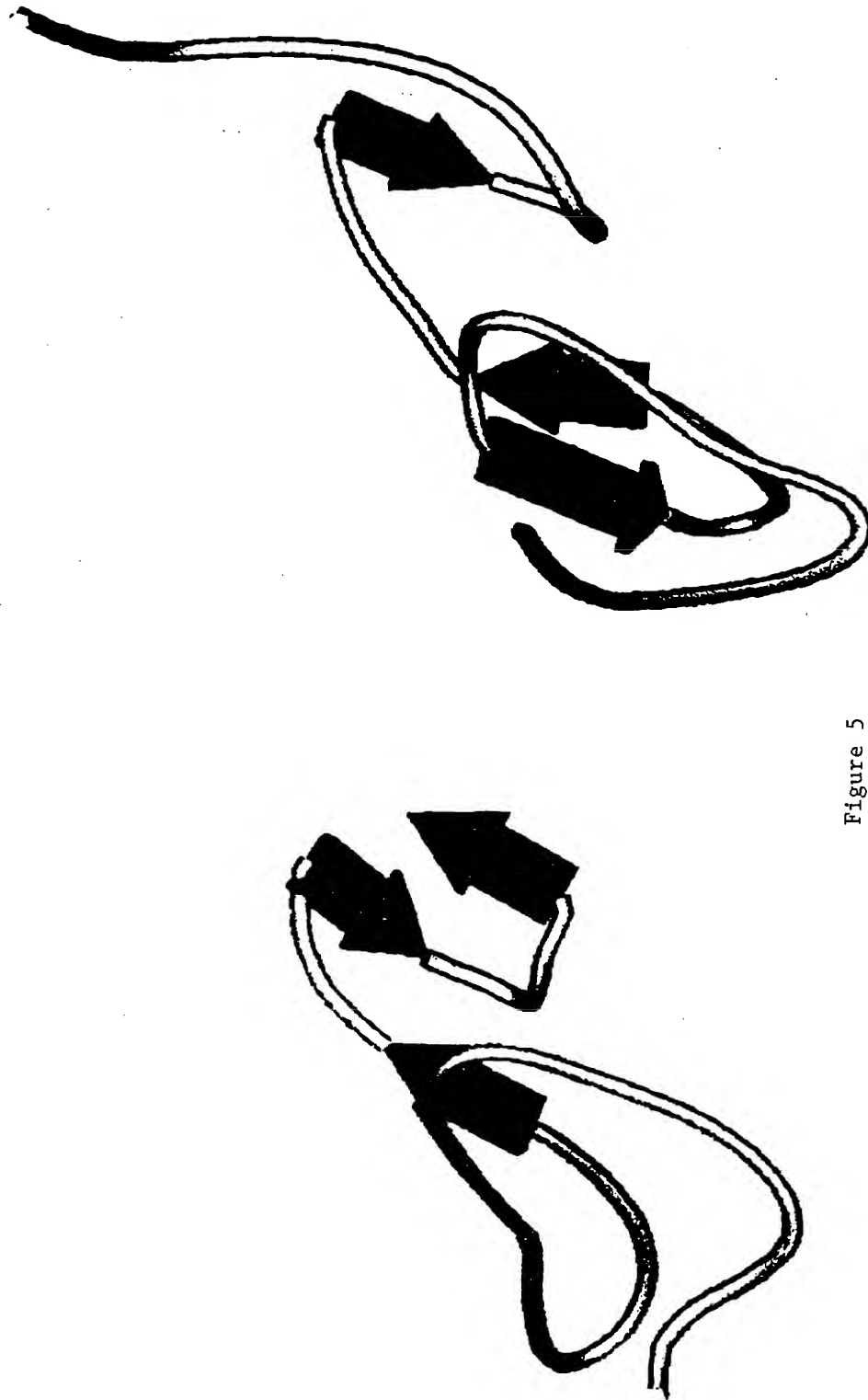


Figure 5